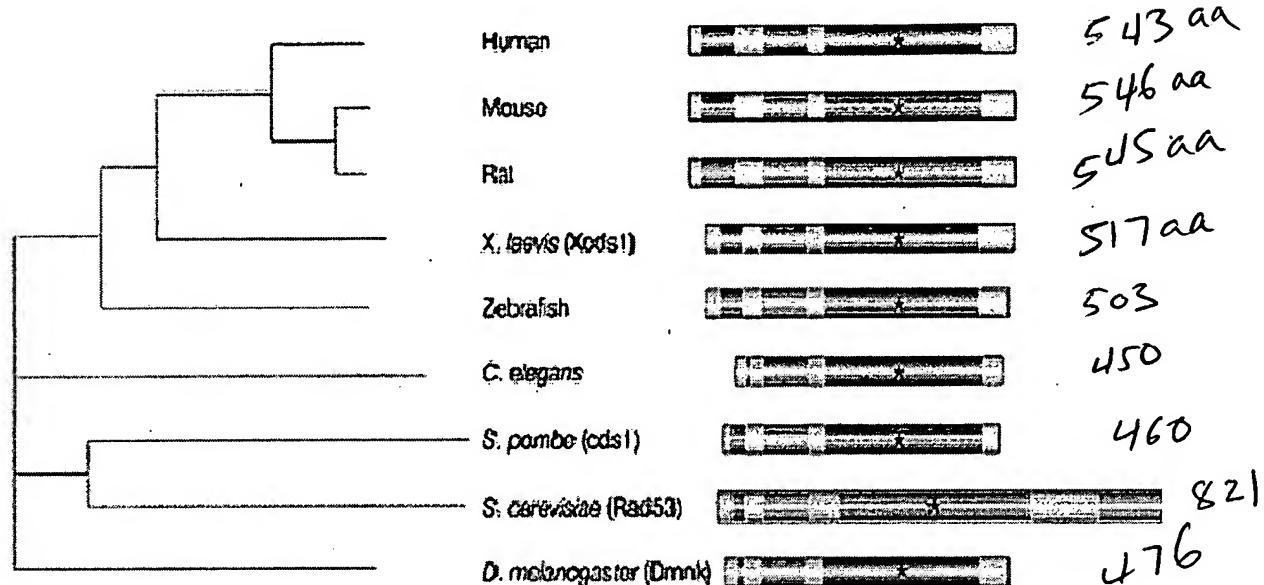




# Chk2 in evolution



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On the left is a phylogenetic tree showing the degree of amino-acid sequence similarity between the Chk2 homologues in different organisms. (The alternative names of Chk2 in some species are indicated in parentheses.) To the right is an alignment of conserved domains in the Chk2 homologues: the SQTQ-rich domain (maroon); the FHA domain (blue); and the kinase domain (brown). The highly conserved activation loop is marked by an asterisk (\*). Amino-acid (aa) sequence accession numbers are: human, AAC83693; mouse, AAC83694; rat, AAD55890; *Xenopus*, AAF75829; zebrafish, AAK52419; *Schizosaccharomyces pombe*, Q09170; *Saccharomyces cerevisiae*, A39616; *C. elegans*, BAB15803; *Drosophila melanogaster*, BAA28755.

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the right is an alignment of conserved domains in the Chk2 homologues: the SQ/TQ-rich domain (maroon); the forkheadassociated

domain (FHA; blue); and the kinase domain (brown). The highly conserved activation loop is marked by an asterisk.

Amino-acid (aa) sequence accession numbers are: human, AAC83693; mouse, AAC83694; rat, AAD55890; *Xenopus laevis*,

AAF75829; zebrafish, AAK52419; *Schizosaccharomyces pombe*, Q09170; *Saccharomyces cerevisiae*, A39616; *Caenorhabditis*

*elegans*, BAB15803; *Drosophila melanogaster*, BAA28755.

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